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Minimum
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1: geneseqp1980s:*
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1047
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480.520 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	σ	ຫ	.4	w	N	_	No.
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90.3	90.3	90.3	90.3	90.3	90.5	93.1	93.1	93.1	93.1	93.1	93.1	93.1	96.6	99.0	99.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match Length
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Adm83852 Human can	Adm83853 Human can	Adm83801 Human can	Adm83808 Human can	Add84545 121P1F1 v	Adm83813 Mouse hyp	Adm83858 Human can	Adm83809 Human can	Adm83803 Human can	Adm83859 Human can	Adm83857 Human can	Add84547 121P1F1 v	Aam40043 Human pol	Adm83814 Human can	Adm83835 Human can	Adm83834 Human can	Abp75541 Human sec	Adm83804 Human can	Adm83811 Human can	Adm83793 Human can	Adm83812 Human can	Adm83810 Human can	Adm83851 Human can	Adj70015 Human hea	Add84537 121P1F1 p	Description

The present invention describes a composition (I) comprising a substance that modulates the status of 121P1F1 (gene and encoded protein), or a molecule that is modulated by 121P1F1, where the status of a cell that expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome 4q. (I) has cytostatic activity, and can be used in gene therapy, and in vaccines. The composition (I) can be used for diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its fragment can be used to elicit a humoral or cellular immune response.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
135.5	255.5	287	329.5	349	465	465	465	465	584	584	584	584	591	591	591	591	591	606	614
12.9	24.4	27.4	31.5	33.3	44.4	44.4	44.4	44.4	55.8	55.8	55.8	55.8	56.4	56.4	56.4	56.4	56.4	57.9	58.6
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Adp26646	Adh32846	Aag74669	Abg12341	Adm83815	Adm83805	Adm83795	Adm83836	Add84539	Adm83837	Adm83806	Adm83797	Add84541	Adm83844	Adm83807	Adm83845	Adm83799	Add84543	Aam41829	Adm83843
Mouse dyn	Yeast smO	Human col	Novel hum	Yeast hyp	Human can	Human can	Human can	121P1F1 v	Human can	Human can	Human can	121P1F1 v	Human can	Human can	Human can	Human can	121P1F1 v	Human pol	Human can

ALIGNMENTS

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition comprising a substance that modulates the status of 121P1F1, useful in diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or lung cancer.
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N-PSDB; ADD84536.
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                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Fig 2A; 285pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitochondrial; human; screening assay; diabetes mellitus; Huntington's disease; osteoarthritis; Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides are useful as probes and primers for the amplification of detection of 121PIT genes, as coding sequences for directing the expression of 121PIT polypeptides, or as tools for modulating or inhibiting the expression of 121PIF1 genes. The present sequence is used in the exemplification of the present invention.
                                                                               Identifying a mitochondrial target for drug screening assays and treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correl
                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2002; 2002US-0372843P
17-JUN-2002; 2002US-0389987P
20-SEP-2002; 2002US-0412418P
     Claim
                                                                                                                                                                                        WPI; 2003-845369/78
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                                                                                      (FARI/)
(AFAR/)
                                                                                                                                             (CHAL/)
(HUBE/)
(RAIT/)
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AFAR D E H.
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Crecombolinant protein comprising an antigen-binding region of a monoclonal CC antibody, a non-human transgenic animal that produces an antibody, a CC hybridoma that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121PIFI-related protein (comprising CC that immunospecifically binds to a 121PIFI-related protein (comprising CC chain monoclonal antibody, a polynucleotide that encodes a single CC chain monoclonal antibody, a polynucleotide that encodes an analogue CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell that expresses 121PIFI, inhibiting growth of cancer cells that expresses CC 121PIFI (comprising administering to the cells the composition), treating a patient who bears cancer cells that express 121PIFI, generating a cresponse, monitoring 121PIFI gene products in a biological sample from a CC mammalian immune response directed to 121PIFI, inducing an immune cresponse, monitoring the CC gresence of a 121PIFI related protein or polynuclectide in a biological sample from a CC generate who has or who is suspected of having cancer, monitoring the CC composition may comprise a polynucleotide that comprises a 121PIFI cancer The composition may comprise a polynucleotide that comprises a 121PIFI cancer the coding sequence does not encode the entire amino acid sequence of 121PIFI (ADM83793. The CC peptide given in 16 Tables (given in the specification), the peptides being HIA (human leukocyte antigen)—binding epitopes from 121PIFI or its splice variants. The composition is useful for detecting, treating or crecer, colon cancer, preferably prostate cancer, bladder cancer, kidney carcine to treat or prevent cancer. The composition can also be used as a vaccine to treat or prevent cancer that expresses or overexpresses concerned to treat or prevent cancer that expresses or overexpresses.
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Best Local Similarity
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Pred. No. 1.5e-88;
0; Mismatches 0;
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RESULT 4

preferably prostate cancer,

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The invention relates to a composition comprising a substance that CC gene) or a molecule that is modulated by 121P1F1 where status of the cell that texpressed sees 121P1F1 is modulated. Also included are a pharmaceutical cc composition comprising the novel composition in a human unit dose form, a crecombinant protein comprising an antipody, a mon-human transgenic animal that produces an antibody, a cancer expresses composition in a human unit dose form, a cream transpenic animal that produces an antibody, a composition of a monoclonal cc that immunospecifically binds to a 121P1F1-related protein (comprising the variable domains of the heavy and light chains of a monoclonal compatition, a vector comprising a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single compatitie, delivering a cytotoxic agent or a diagnostic agent to a cell that expresses clipped (comprising administering to the cells the composition), treating a patient who has cryotoxic agent to a cancer cells that expresses clipped (comprising administering to the cells the composition), treating a patient who has or who is suspected to having cancer, monitoring the composition may comprise a polynucleotide that comprises a lipped the composition may comprise a polynucleotide that comprises a lipped cancer. The composition of may comprise a polynucleotide that the coding sequence does not encode the entire amino acid sequence of 121P1F1 (ADM83793. The substance also comprises a polynucleotide that encodes at least one composition in the specification), the peptides being Hila (human leukocyte antigen)-binding epitopes from 121P1F1 or its splice variants. The composition is usef
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(RAIT/)
(FARI/)
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JAKOBOVITS A.
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HUBERT R S.
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Best Local
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                     creating or lung cancer.
                                   New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                 WPI; 2004-060522/06
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                                                                                                                   Challita-Eid PM,
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(HUBE/)
(RAIT/)
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Disclosure;

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RESULT 6 ADM83793

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standard;

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Human 03-JUN-2004

cancer

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121P1F1 protein

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entry

Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; human leukocyte antigen; prostate cancer; bladder cancer; kidne colon cancer; lung cancer; pancreatic cancer; breast cancer;

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Best Local
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Pred. No. 1.5e-88;
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cervical cancer;

stomach cancer; gene therapy; vaccine

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composition may comprise a polynucleotide that composition and immune response (2018) the expresses (2018) the colls that expresses (2018) that expresses (2018) that expresses (2018) that expresses (2018) the colls the composition), treating a patient who bears cancer cells that express (2018) the composition immune response directed to (21818), inducing an immune response, monitoring (1218) as patient who has or who is suspected of having cancer, monitoring the presence of cancer in an individual and an assay for detecting the presence of a (1218) related protein or polynucleotide in a biological sample from a gatient who has or who is suspected of having cancer. The composition may comprise a polynucleotide that comprises a (21818) related protein coding sequence provided that the coding sequence does not encode the entire amino acid sequence of (1218) (ADM83793). The substance also comprises a polynucleotide that encodes at least one peptide given in 16 Tables (given in the specification), the peptides splice variants. The composition is useful for detecting, treating or cancer, colon cancer, preferably prostate cancer, bladder cancer, kidney cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a hybridoma that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121P1F1-related protein (comprising the variable domains of the heavy and light chains of a monoclonal
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N-PSDB; ADM83792.
cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer, cervical cancer or stomach cancer. The composition can also be used as vaccine to treat or prevent cancer that expresses or overaxpresses 121PIF1. The gene for 121PIF1 is located on chromosome 4q. The present sequence is a 121PIF1 protein (full-length or fragment).
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JAKOBOVITS A.
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Query Match Best Local Similarity

100

Score Pred.

1047; DB 8; No. 1.5e-88;

Length 205

Sequence 205

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ARRSULT 7
ALMWSJET 7
ALMWSJET 8
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The invention relates to a composition comprising a substance that modulates the status of 121P1F1 (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121P1F1 where status of the cell that expresses 121P1F1 is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a hybridoma that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121P1F1-related protein (comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HI human leukocyte antigen; prostate cancer; bladder cancer; kidney colon cancer; lung cancer; pancreatic cancer; breast cancer; cervical cancer; stomach cancer; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                             Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
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(HUBE/)
(RAIT/)
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HUBERT R S.
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RESULT
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CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
CC 121P1F1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121P1F1, generating a
CC mammalian immune response directed to 121P1F1, inducing an immune
CC meaning 121P1F1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121P1F1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121P1F1-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121P1F1 (ADM83793. The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides
CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, preferably prostate cancer, breast cancer, kidney
CC cancer, colon cancer or stomach cancer. The composition can also be used as a
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC reminer is a 121P1F1 protein (full-length or fraement)
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Best Local :
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cervical cancer; st
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28-FEB-2002; 2002US-00087190
                                                                   04-DEC-2003
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                                                                                                                                                                                                                                                                                        cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
cancer; lung cancer; pancreatic cancer; breast cancer;
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                                                                                                                                                                                                                                                             stomach cancer; gene therapy; vaccine.
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smatches 0;
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MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV

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120 60 60

120

121 19

TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180

Best Loc Matches

Local

Similarity

1.5e-88;

Indels

0;

Gaps

0

Conservative

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The invention relates to a composition comprising a substance that comboulates the status of 121P1F1 (a protein encoded by a cancer expressed composition or a molecule that is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal composition protein comprising an antigen-binding region of a monoclonal combrided, a non-human transgenic animal that produces an antibody, a function of the heavy and light chains of a monoclonal antibody, a vector comprising a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single composition of the variable domains of the heavy and light chains of a monoclonal composition of the variable domains of the heavy and light chains of a monoclonal antibody, a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes a single composition of the variable domains of the cells the composition), treating a polynucleotide that encodes a single composition of the composition of the cells that expresses 121P1F1, generating a polynucleotide that encodes an analogue composition mumner response directed to 121P1F1, inducing an immune composition may comprise a polynucleotide in a biological sample from a patient who has or who is suspected of having cancer. The composition may comprise a polynucleotide that comprises a 121P1F1.

Cc sample from a patient who has or who is suspected of having cancer. The composition and polynucleotide that encodes at least one composition and polynucleotide that encodes at least one composition is useful for detecting, treating or its substance also comprises a polynucleotide that encodes at least one composition is useful for detecting, treating or its splice variants. The composition is useful for detecting, treating 
                                                Query Match
                                                                                                                                     cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer, cervical cancer or stomach cancer. The composition can also be used as vaccine to treat or prevent cancer that expresses or overexpresses 121PlF1. The gene for 121PlF1 is located on chromosome 4q. The present sequence is a 121PlF1 protein (full-length or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 14; 211pp; English
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AFAR D E H.
GE W.
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29-MAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299776P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; Cell proliferative disorder; anti-inflammatory; immunosuppressive; neuroprotective; nootropic; neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic; antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus; secretory polynucleotide; secretory protein.
The invention relates to a secretory polynucleotide (designated sptm) comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a naturally occurring polynucleotide sequence at least 90 % identical to the polynucleotide sequence at least 90 % identical to the polynucleotide sequence at polynucleotide are useful for RNA equivalent of them. The polynucleotide or polynucleotide are useful for treating, preventing or diagnosing a disease or condition associated with the expression of functional SPTM. These are particularly useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's disease), neurological disorders (e.g. epilepsy, Huntington's disease, dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
                                                                                                                                                                                                                                                                                                                                                                         Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen w, Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PB, Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleeft Peralta CH, David MH, Lewis SA, Chen AJ, Panze: Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                           New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or
                                                                                                                                                                                                                                                                                                                                   WPI; 2003-075543/07.
N-PSDB; ABZ35987.
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                                                                                                                                                                                                              Claim 27;
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O, Yap PE, A
DA, Kleefeld
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                                                                                                                                                                                                                                                                                                         cervical
                                                                                                                                                                                                                                                                                                                   Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA; human leukocyte antigen; prostate cancer; bladder cancer; kidney ca colon cancer; lung cancer; pancreatic cancer; breast cancer;
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                                                       Challita-Eid
Jakobovits A;
                                                                                                                         (HUBE/)
(RAIT/)
(FARI/)
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(GEWW/)
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GEW.
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                                                                                                                                                             CHALLITA-BID P
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                                                                                                                                                                                                                                                                                                          cancer;
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                          stomach
                                                                    Hubert
                                                                  RS,
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New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,

WPI; 2004-060522/06

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RESULT 11
ADM83835
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Best Local :
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                                                                                      03-JUN-2004
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           gene 121P1F1 variant protein
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Pred. No. 1.4e-87;
0; Mismatches 0;
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human leukocyte antigen; prostate cancer; bladder cancer; kidney colon cancer; lung cancer; pancreatic cancer; breast cancer; cervical cancer; stomach cancer; gene therapy; vaccine.
                      Challita-Eid PM, Hubert RS,
                                                                                                                                                        (CHAL/)
                                                                                                                                                                                                                                                                                                04-DEC-2003
Jakobovits A;
                                                                                                                                                                                                                 08-FEB-2001; 2001US-00779250.
                                                                                                                                                                                                                                                         28-FEB-2002; 2002US-00087190.
                                                                                                   (AFAR/)
                                                                                                                                          (RAIT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer gene 121P1F1; cytostatic; cancer; chromosome 4q;
                                                                           AFAR DEH.
GEW.
                                                                                                                                                        CHALLITA-BID P M.
HUBERT R S.
                                                            JAKOBOVITS
                                                                                                                   FARIS M.
                                                                                                                                      RAITANO A B.
                      Raitano AB, Faris M,
                      Afar DEH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HĽA;
                      Ge W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
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New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or lung cancer.

WPI; 2004-060522/06.

Example 5; SEQ ID NO 45; 211pp; English.

Commodulates the status of 121PIF1 (a protein encoded by a cancer that modulates the status of 121PIF1 (a protein encoded by a cancer expressed composition comprising the novel composition included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a crecombinant protein comprising an antigen-binding region of a monoclonal cantibody, a non-human transgenic animal that produce an antibody, a that immunospecifically binds to a 121PIF1-related protein (comprising the novel composition) that immunospecifically binds to a 121PIF1-related protein (comprising the variable domains of the heavy and light chains of a monoclonal antibody, a vector comprising a polymucleotide that encodes a single chain monoclonal antibody, a polymucleotide that encodes a cell chair expresses 121PIF1, inhibiting growth of cancer cells that expresses that expresses cancer cells that expresses cell that expresses cancer cells that expresses cell that expresses cancer cells that expresses cell that ex

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ADM83814
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Best Local Similarity
Matches 205; Conser
The invention relates to a composition comprising a substance that modulates the status of 121P1F1 (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121P1F1 where status of the cell that expresses 121P1F1 is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human leukocyte antigen; prostate cancer; bladder cancer; ki-
colon cancer; lung cancer; pancreatic cancer; breast cancer;
cervical cancer; stomach cancer; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM83814 standard;
                                                                                                                        New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                                                                                                                                  Challita-Eid
Jakobovits A;
                                                                                                                                                                                                                                                                                                                                         08-FEB-2001; 2001US-00779250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cancer gene 121P1F1 protein fragment.
                                                                                                                                                                            WPI;
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                                                                                      Example
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GEW.
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                                                                                                                                                                                                                                                                                                                  CHALLITA-EID P M.
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                                                                                      SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; 198
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Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibody), a vector comprising a polynucleotide that encodes a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody, a non-human transgenic animal that produces an antibody,
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  121
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KELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKF
                                                                                                                                                                   IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLA
                                                                                                              IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLA
                                                                                                                                                                                                                         KGLSAEEKRTRMME1FSETKDVFQLKDLEK1APKEKG1TAMSVKEVLQSLVDDGMVDCER
                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                           96.6%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                     Length 198;
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181
              185
              GFEENKIDRTFGIPEDFD
GFEENKIDRTFGIPEDFD
              202
198
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RESULT 13 AAM40043

AAM40043 standard; protein; 190 A

22-OCT-2001 (first entry)

TX6XFXEXEXEXEXEXEXEXEXE Human polypeptide SEQ ID NO 3188.

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; neuropathy; central nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; cancer;

chemokinetic; thrombolytic; eukaemia.

Homo sapiens.

WO200153312-A1

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RESULT 14
ADD84547
ID ADD84
XX
AC ADD84
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Best Local
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21-JAN-2000;
25-APR-2000;
25-JUN-2000;
20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang
Wang
                              ADD84547 standard; protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                                              Sequence 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001.
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                      of the printed specification
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DB; AAI59199.
                                                                                                    181
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                                                                                                                                                                                                                                                                                                                         190;
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Wang Z,
Goodrich
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                                                                                                                                                                                                            SKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE
                                                                                                                                                                                                                                                                   MMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNYYWAFP
                                                                                                                                                       QLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTF
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; 2000US-00552317.

; 2000US-00598042.

; 2000US-00620312.

; 2000US-00623450.

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Wehrman T,
h R, Drmanac
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100.0%;
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Xu C,
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Yang Y,
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Zhang J,
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                                                                                                                                                                                                                                                                                            The present invention describes a composition (I) comprising a substance CC that modulates the status of 121PIF1 (gene and encoded protein), or a molecule that is modulated by 121PIF1, where the status of a cell that cexpresses 121PIF1 is modulated. The human 121PIF1 gene maps to chromosome 4q. (I) has cytostatic activity, and can be used in gene therapy, and in vaccines. The composition (I) can be used for diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121PIF1, such as breast, colon, ovarian or lung cancer. The 121PIF1 gene or its fragment can be used to elicit a humoral or cellular immune response. 121PIF1 antibodies can be used in active or passive immunisation. 121PIF1 polypoptides, or as tools for modulating or inhibiting the expression of 121PIF1 polypoptides, or as tools for modulating or used in the exemplification of the present invention.
                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                            Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
Homo sapie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition comprising a substance that modulates the status of 121PIF1, useful in diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121PIF1, such as breast, colon, ovarian or lung cancer.
                                                                                                                                                                                                                                                                                            Sequence 190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 19; Fig 2F; 285pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ADD84546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Challita-Eid PM, Hubert RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAR-2001; 2001US-00799250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic; qene therapy; vaccine; cancer; immune response; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2002; 2002WO-US006242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200295009-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2004
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                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-156757/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
                                     121
                                                                     136
                                                                                                  61
                                                                                                                                76 SKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE 135
                                                                                                                                                                                   16 MMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNYYWAFP
GIPEDFDYID
                                     QLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTF
                                                       QLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTF
                                                                                                  SKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE
                                                                                                                                                                 MMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNYYWAFP
                                                                                                                                                                                                                              Conservative
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      205
                                                                                                                                                                                                                                           93.1%;
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                                                                                                                                                                                                                                             Score 975;
Pred. No.
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                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                         6.3e-82;
                                                                                                                                                                                                                                                           DB
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                                                                                                                                                                                                                                                             7;
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181

GIPEDFDYID

190

120

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0

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RESULT 15
ADM83857
  composition comprising the movel composition in a human unit dose form, a crecombinant protein comprising an antigen-binding region of a monoclonal cantibody, a non-human transgenic animal that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121P1F1-related protein (comprising the variable domains of the heavy and light chains of a monoclonal antibody that immunospecifically binds to a 121P1F1-related protein (comprising the variable domains of the heavy and light chains of a monoclonal antibody and polymucleotide that encodes a single chain monoclonal antibody, a polymucleotide that encodes an analogue peptide, delivering a cytotoxic agent or a diagnostic agent to a cell that expresses 121P1F1, inhibiting growth of cancer cells that expresses 121P1F1 (comprising administering to the cells the composition), treating a patient who bears cancer cells that expresses 121P1F1, prinducing an immune response directed to 121P1F1, inducing an immune creponse directed to 121P1F1, inducing an immune creponse, monitoring 121P1F1 gene products in a biological sample from a patient who has or who is suspected of having cancer, monitoring the presence of al21P1F1-related protein or polymucleotide in a biological sample from a patient who has or who is suspected of having cancer. The composition may comprise a polymucleotide that tomprises a 121P1F1 (and sequence does not encode the entire amino acid sequence of 121P1F1 (ADM83793). The substance also comprises a polymucleotide that encodes at least one composition and matical actions in the specification, the peptides of the composition in the specification, the peptides of the composition and the substance and the substance of 121P1F1 (ADM83793). The substance also comprises a polymucleotide that encodes at least one composition and substance in the specification, the peptides of the composition of the substance in the substance of 121P1F1 (ADM83793). The substance of 121P1F1 (ADM83793).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a composition comprising a substance that modulates the status of 121PIFI (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121PIFI where status of the cel that expresses 121PIFI is modulated. Also included are a pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer gene 121P1P1; cytostatic; cancer; chromosome 4q; HI human leukocyte antigen; prostate cancer; bladder cancer; kidney colon cancer; lung cancer; pancreatic cancer; breast cancer; cervical cancer; stomach cancer; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; SEQ ID NO 67; 211pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Challita-Eid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001; 2001US-00779250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2002; 2002US-00087190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer.
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GEW.
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FARIS M.
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(human leukocyte antigen)-binding epitopes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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121P1F1 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA;
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                                                                                                                                                                                                                                                                            Matches 190;
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                           splice variants. The composition is useful for detecting, treating or preventing cancer, preferably prostate cancer, bladder cancer, kidney cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer, cervical cancer or stomach cancer. The composition can also be used as vaccine to treat or prevent cancer that expresses or overexpresses 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present sequence is a 121P1F1 protein (full-length or fragment).
                                                                                                                                                                                                                                                                                                                                              Sequence 190 AA;
                                                                                                                                                                                                                                                                                              Local Similarity
181
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                                                                                                    136
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                                                                                                                                                        SKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE
                                                                                                                                                                                                                                     MMEIFSETKOVFQLKOLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNYYWAFP
                                                                                         QLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTF
GIPEDFDYID
                                  GIPEDFDYID 205
                                                                  QLKABVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTF
                                                                                                                                    SKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE
                                                                                                                                                                                                          MMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNYYWAFP
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                          93.1%;
                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                            Score 975; DB 8;
Pred. No. 6.3e-82;
                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                            Length 190
                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                            Gaps
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Search completed: July 27, 2005, 09:37:57 Job time: 166 secs

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GenCore version 5.1.6

	Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - pro	OM protein - protein search, using sw model
Run on:	July 27, 2005, 09:28:34 ; Search time 40 Seconds (without alignments) 493.111 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-087-190-3 1047 1 MSKKKGLSAEEKRTRMMEIFFEENKIDRTFGIPEDFDYID 205
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416

283416 segs, 96216763 residues

Searched:

Minimum DB Maximum DB seq geq length: 0 length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10 Listing first 45 summaries 100%

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution. printed,

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	თ	_υ	4	ω	2	1	Result No.
109	109.5	109.5	109.5	109.5	109.5	109.5	110	110.5	110.5	110.5	111	111	112	112	112	112	113	114	114	115.5	116.5	117	121.5	•	135.5	168.5	197	349	Score
10.4	10.5	10.5		10.5		10.5	0	0	0	10.6	10.6	10.6	10.7	10.7	10.7	10.7	10.8	.10.9	10.9	11.0	11.1	11.2	11.6	12.5		16.1	18.8		Query Match I
284	1390	1298	400	284	168	168	284	879	629	308	1937	559	1938	559	285	284	199	764	284	880	2442	768	1356	1053	1281	174	128	210	Length [
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	BB
JC2551	S51364	T24480	E70318	JC6198	B72046	G86578	I51731	C71083	T44607	T08796	I38055	A45620	A59293	S49143	A24199	JC6199	A32183	T05409	S24972	F75103	T08621	T02572	S32763	A41642	JC5368	S61134	T08972	76	ID
tropomyosin aipna	sperm tail-specifi	hypothetical prote	hypothetical prote	alpha-tropomyosin	conserved hypothet	CT670 hypothetical	alpha-tropomyosin	conserved hypothet	hypothetical prote	tropomyosin - huma	myosin heavy chain	cytovillin homolog	skeletal myosin he	EG10 protein - tap	tropomyosin NM, sk	alpha-tropomyosin	tropomyosin TPM1 -	hypothetical prote	tropomyosin alpha,	conserved hypothet	centrosome associa	hypothetical prote	kinectin 1 - human	dynactin - chicken	•	•	hypothetical prote	ical	Description

A; Molecule type: DNA

RESULT 2 T08972

RESA-H3 antigen PF	B71603	2	1558	10.1	106	5
myosin II heavy ch	T47237	N	746	10.2	106.5	4
myosin heavy chain	S24348	N	955	10.2	107	ັພ
tropomyosin 2, fib	A60597	N	284	10.2	107	2
tropomyosin alpha	A25825	N	284	10.2	107	Ξ
tropomyosin alpha	B27407	N	284	10.2	107	5
tropomyosin 2, fib	A39816	N	284	10.2	107	9
tropomyosin alpha	TMRBA	<u> </u>	284	10.2	107	<u>8</u>
tropomyosin 1 alph	A34787	N	281	10.2	107	7
tropomyosin alpha	A22165	N	280	10.2	107	9
P115 homolog - Met	A64505	N	1169	10.3	107.5	ັກ
hypothetical prote	T19414	N	1137	10.3	107.5	4
hypothetical prote	F96712	N	1085	10.3	107.5	$\bar{\omega}$
hypothetical prote	F84899	N	670	10.3	108	ឆ
myosin heavy chain	S00084	N	676	10.4	109	Ξ
tropomyosin alpha,	S19691	N	284	10.4	109	õ

ALIGNMENTS

hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T37610 R;Hunt, S.; Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, submitted to the EMBL Data Library, September 1995 A;Reference number: Z21730 á 밁 Ś 밁 δ 밁 S A;Cross-references: UNIPROT:Q09739; EMBL:Z54096; PIDN:CAA90804.1; GSPDB:GN00066; SPDB:SPA;Experimental source: strain 972h-; cosmid c13A11 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-210 <HUN> A; Map position: A; Introns: 22/3 A; Gene: SPDB: SPAC13A11.03 A; Accession: T37610 Query Match Best Local S Matches 84 Genetics: y Match 33.3%; Score 349; DB 2; Length 210; Local Similarity 41.6%; Pred. No. 3.9e-16; ndels 84; Conservative 36; Mismatches 76; Indels 183 181 123 122 63 83 4 5 KGLSABEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER KGLSLAEKRRKLEAIFHDSKDFFQLKEVEKLGSK-KQIVLQTVKDVLQSLVDDNIVKTEK 62 KRKFGFEENKIDRTFGIPEDFD 202 OYTLELLHAKESELKLIKTQLSNLNHCNPETFELKNENTKKYMEAANLWTDQIHTLIAFC 182 RLAKELSSLRD-QREQLKAEVEKYKDCDPQVVEBIRQANKVAKEAANRWTDNIFAIKSWA 180 IGTSNYYWSFPSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTENDAN 122 IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI--EKAKIGRCETE-ERT 121 -RDMGADTNOIREYCSIPEDLD 203 6. Gaps 64 s.v.

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N;Alternate names: nypouncular C. Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004 C;Accession: S61134; S64200 R;Bertani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Bruschi, C.V. submitted to the EMBL Data Library, September 1995 A;Description: The sequence analysis of a 7.9 kb DNA fragment from the left ive new genes.
RESULT
JC5368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-128 <BEV>
A;Cross-references: UNIPROT:Q9SZE5; EMBL:AL078470; GSPDB:GN00062; ATSP:F19B15.200
A;Experimental source: cultivar Columbia; BAC clone F19B15
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cros
A;Map
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A; Residues: 1-174 <BER>
A; CRESIDUES: 1-174 <BER>
A; CROSS-references: UNIPROT: P53102; EMBL: X91489; NID: g1143557; PIDN: CAA62791.1;
R; Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Deineri,
R; Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Deineri,
Submitted to the Protein Sequence Database, May 1996
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A;Residues: 1-174 <BRU>
A;Cross-references: EMBL:Z72705; NID:gl322796; PIDN:CAA96895.1; PID:e243495; PID:gl3227:
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S64183
A; Accession: S64200
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A;Map position: 4
A;Introns: 13/3; 52/3; 88/3; 109/3
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Best Local
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49; Conserv
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                                                                            QENKQQIRLKKVHLEKTTDNIEILIDYLYKKFFLKPEQIRKEFGIPEEF
                                                                                                                  QANK----VAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTFGIPEDF 201
                                                                                                                                                            KOELDKTLATGRRKKFTVGQKSYNREALLEKRKKIQDEIKK-KSNSLQKIESIRWDAAKI
                                                                                                                                                                                                                                          MIVKDLVQQMIDEDGVISVEKCGNINIYWCFKNQTLQKLYDSSELIKKKIQEVKCDIATY
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Pred. No. 0.00021
2; Mismatches 6
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Pred. No. 2e-06;
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dynactin 1 - mouse
N;Alternate names: p150 Glued
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-May-197 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5368
C;Accession: JC5368
R;Jang, W.; Weber, J.S.; Tokito, M.K.; Holzbaur, E.L.F.; Meisler, M.H.
Biochem. Biophys. Res. Commun. 231, 344-347, 1997
A;Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate for th A;Reference number: JC5368; MUID:97223454; PMID:9070275
A;Accession: JC5368
A;Molecule type: mANA
A;Residues: 1-1281 cJAN>
A;Residues: 1-1281 cJAN>
A;Residues: 1-1281 cJAN>
A;Residues: This protein is a member of the oligomeric dynactin complex that is required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Gallus gallus (chicken)
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
C;Accession: A41442
C;Accession: A41442
R;Gill, S.R.; Schroer, T.A.; Szilak, I.; Steuer, E.R.; Sheetz, M.P.; Cleveland, D.W.
J. Cell Biol. 115, 1639-1650, 1991
A;Title: Dynactin, a conserved, ubiquitously expressed component of an activator of
                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Restdues: 1-1053 <GIL>
A;Cross-references: UNIPROT:P35458; GB:X62773; NID:g63920; PID:g63921
C;Keywords: cytoskeleton
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A; Map position:
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                                                                                161 LEILKHEIEEKGSDGAASSYQVKQLEEQNARLKEALVRMRDLSASEKQEHVKLQKQMEKK
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                                         KIGRCETEERTRLAKELSSLRDQREQLKAEVEK-YKDCD-----
                                                                                                                         GMV----DCERIGTSNYYWAFPSKALHARKHKLE----VLESQLSEG-SQKHASLQKSIEKA 110
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TELESLROOREKLOEEVKQAEKTVDELKEQVDAALGAEEMVETLTE
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                                                                                                                                                                                                                                                                        Score 130.5; Di
Pred. No. 0.46;
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158

ANKVAKEAANRWTDNI FAIKSWAKRKFGFEENKIDRTFGIPEDFD

202

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hypothetical protein At2g39300 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T16B24.6
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02572; R84815
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.;
submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
A;Reference number: Z14679
A;Raccession: T02572
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-768 <ROU>
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A; Title: Molecular cloning and characterization of human A; Reference number: 137947; MUID:95308853; PMID:7787243
A; Accession: 137947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence
C;Accession: S32763; I37947
R;Kruppa, G.; Fuetterer, A.; Lemke, H.; Kroenke, M.
submitted to the EMBL Data Library, April 1993
A;Description: Cloning and characterization of TAF, a novel tran A;Reference number: S32763
A;Accession: S32763
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A; Residues: 1-1356 < RES>
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A;Cross-references: UNIPROT:Q86UP2; EMBL:Z22551
A;Cross-references: UNIPROT:080951; EMBL:AC004697; NID:g3402671; PID:g3402677
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
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Pred. No. 2.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
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                                  C.Y.;
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A; DEGLUS. F-TE: DNA
A;Molecule type: DNA
A;Residues: 1-768 <STO>
N.Cross-references: GB:AE002093; NID:g3402677; PIDN:AAC28980.1; GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     euss, D.; Nierman, W.C.; White, Nature 402, 761-768, 1999
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A;Residues: 1-2442 <MAC>
A;Cross-references: EMBL.AF022655; NID:g2832236; PIDN:AAC06349.1; PID:g2832237
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Autoantibodies to a group of centrosomal proteins A;Reference number: Z16462; MUID:98165428; PMID:9506584 A;Accession: T08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Mack, G.J.; Rees, J.; Sandblom, O.; Balczon, Arthritis Rheum. 41, 551-558, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 centrosome associated protein CEP250 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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A; Introns: 80/2;
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                                                                                                                                           1714 KGPSKAQRGSLEHMKLILRDKEKEVECQQEHIHELQELKDQLEQQLQGLHRKVGET----
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ALQQEQQQAQGQEERVKEKADALQGALEQAHMTLKERHGELQDH----KEQARR 1870
                                 SLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKR
                                                                       ---SILLSQREQEIVVLQQQLQEAREQGELKEQSLQSQLDEAQRALAQRDQ-----ELE
                                                                                                         AFPSKALHARKHKLEVLESQLSE----GSQKHASLQKSIEKAKIGRCETEERTRLAKELS
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ilarity 19.7%;
Conservative 4
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22.1%;
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Pred. No. 9.4;
47; Mismatches
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c;Species: Sus scrofa domestica (domestic pig)
c;Species: Sus scrofa domestica (domestic pig)
c;Date: 20-Feb-195 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
c;Dates: Sol-Feb-195 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
c;Accession: S24972
c;Accession: S24972
R;Whitby, F.G.; Kent, H.M.; Stewart, F.; Stewart, M.; Xie, X.; Hatch, V.; C;
R;Whitby, F.G.; Kent, H.M.; Stewart, F.; Stewart, M.; Xie, X.; Hatch, V.; C;
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S24972
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A;Description: Structure of tropomyosin at 9 Angstroms resolution.
A;Reference number: S24972
A;Accession: S24972
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-880 <KAW>
A;Cross-references: UNIPROT:Q9UZC8; GB:AJ248286; GB:AL096836;
                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P42639; EMBL:X66274; NID:g1926; PIDN:CAA46986.1; PID:g1927 C;Superfamily: tropomyosin C;Keywords: cardiac muscle; heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: PAB0812
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein
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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F75103
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A; Residues: 1-284 <WHI>
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Best Local S
Matches 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 LVDDGMVDCERIGTSNYYWAFPSKAL-----HARKHKLEVLESQLSEGSQKHASL---
                       58
                                                                73
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                                                              LAEKKATDAEADVASLNRRIQLFEEELDRAQ----ERLA-----TALQKLEEAEKAADE
                                                                                                       MSKKKGLSAE---EKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNERMKAIEELRKAKGKCPVCGRELTEEHK--KELMERYTLEIKKIEEELKRTTE-EERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEELEDAKQVQKQIERLKARLKGLSPGEVIEKLESLEKERTEIEEAIKEITTRIGQMEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --DEYESKLRRLEKELSKWESELKAIEEVIKEGEKKKERAEEIREKLSEIEKRLEELKPY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKKGL------SAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482
-GMVDCERIGTSNYYWAFPSKALHAR----KHKLEVLESQLSEGSQKH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QKSIEKAK------IGRCET--EERTRLAKELSSL-----RD
                                                                                                                                                                 10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 115.5; ; Pred. No. 3.6; 38; Mismatches
                                                                                                                                                37;
                                                                                                                                                                 Score 114; DB
Pred. No. 1.3;
                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .6;
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                                                                                                                                                                                     2; Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78;
                                                                                                                                                61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                74;
                                                                                                                                              Gaps
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                       100
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hypothetical protein F10M6.170 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C.Pate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #t/C.Paccession: T05409 C.Paccession: T05409 R.Bevan, M.; Weichselgartner, M.; Fartmann, B.; Grande
A;Accession: S53899
A;Molecule type: DNA
A;Residues: 1-199 <POE>
A;Cross-references: EMBL:X86470;
R;Poehlmann, R.; Philippsen, P.
                                                                                                                                                                                                                                                                                                                                      tropomyosin TPM1 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein N2332; protein YNL079c C;Species: Saccharomyces cerevisiae C;Date: 08-Sep-1999 #sequence revision 08-Sep-1989 C;Accession: A32183; S53899; S63011; S63018; S63928
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
A32183
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T05409
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                                                                                                                           A;Cross-references: UNIPROT:P17536; R;Poehlmann, R.; Philippsen, P. submitted to the EMBL Data Library,
                                                                                                                                                                                        A;Accession: A32183
A;Molecule type: DNA
A;Residues: 1-199 <LIU>
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A; Note: F10M6.170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: Z154
A;Accession: T05409
A;Molecule type: DNA
A;Residues: 1-764 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Bevan, M.; Weichselgartner, M.; submitted to the Protein Sequence
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                                                                                                                                                                                                                                                       A; Title: Disruption of the single tropomyosin gene in yeast results A; Reference number: A32183; MUID:89195234; PMID:2649250
                                                                                                                                                                                                                                                                                                 R;Liu, H.; Bretscher, A. Cell 57, 233-242, 1989
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A;Experimental source: cultivar Columbia; BAC clone F10M6
                                                                                                      A; Reference number: S53896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 ERTRLAKELSSLRDOREOLKAEVEKYKDCDPOVVEEIROANKVAKEAANRWTDNIFAIKS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 LHDAERKLLSD------KNKLNRAKEELEKREKTISEASLKHESLQEELKRANV---ELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 MVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 SAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEK-----GITAMSVKEVLQSLV--DDG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WAKR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQAREIEELKHKLRERDEERAALQSSLTLKEEELEKMRQ-----EIANRSKEVSMAISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAESANVLFDKLFARTHRLERQTNQHSVYPDDDDDLPYSNLGVLESDLEAALVALLKREED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVARKLVIIESDLERAEERAELSEGKC-----AELEEELKTVTNNLKSLEAQAEKYSQKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.9%;
                                                                                                                                                                                                                                                                                                                                          e_revision 08-Sep-1989 #text_change
S63011; S63018; S63928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                       NID: 9791101; PIDN: CAA60179.1;
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Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 114;
Pred. No. 3
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                                                                                                                           April 1995
                                                                                                                                                                       EMBL: M25501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B.; Granderath, K.; Dauner, D.; Herzl, A.; February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                       NID:g173037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 764;
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                                                                                                                                                                         PIDN: AAA35174.1;
                       PID:g791105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                                                                                                                                       PID:91730
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RESULT 13
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A;Residues: 1-199 <POW>
A;Residues: 1-199 <POW>
A;Cross-references: EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; MIPS:YNL07
A;Experimental source: strain S288C
A;Experimental source: strain S288C
B;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63018
A;Accession: S63018
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-284 <LUQ>
A;Cross-references: UNIPROT:P87349; GB:U33450; NID:g1871357; PIDN:AAC60092.1; PID:g1871
C;Comment: This protein is a actin-binding protein.
C;Genetics:
C;Genetics: ATmS-1
C;Superfamily: tropomyosin
C;Keywords: actin binding
                                                                                                                                                                                                      R;Luque, E.A.; Spinner, B.J.; Dube, S.; Dube, D.K.; Lemanski, L.F. Gene 185, 175-180, 1997
A;Title: Differential spression of a novel isoform of alpha-tropomyosin in A;Reference number: JC6198; MUID:97208870; PMID:9055812
A;Contents: skeltal muscle
A;Accession: JC6199
                                                                                                                                                                                                                                                                                                                                                           C;Species: Ambystoma mexicanum (axolotl)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC6199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Residues: 1-199 - FOF>
A,Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                             alpha-tropomyosin S-1 - axolotl C; Species: Ambystoma mexicanum
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C; Superfamily: tropomyosin TPM1
C; Keywords: coiled coil; cytosk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome A; Reference number: S63925; MUID:96267764; PMID:8701611
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Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-reterences:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues: 1-199 <SOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 DPQVVE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 HASLQKSIBKAKIGRCETEERTR-----LAKELSSLRDQREQLKAEVE----KYKDC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 KKELDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NQQLEEDLEESDTKLKETTEKLRESDLKADQLERRVAALEEQREEWERKNEELTVKYEDA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEAESWOEKYEELKEKNKDLEO-ENVE----KENOIKSLTVKN--OOLEDEIEKLEAGLS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSKQTEQDNVEKENQIKSLTVKNHQLEEEIEKLEAELAESKQLSEDSHHLQSNNDNFSKK 125
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S62997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.8%; Score 113; 24.7%; Pred. No. 1;
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RESULT 15 S49143

EG10 protein - tapeworm C; Species: Echinococcus

(Echinococcus granulosus

granulosus)

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A;Title: Organization of the hTM(nm) gene. A;Reference number: S02554; MUID:88332987; A;Accession: S06210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-285 < CLA>
A; Residues: 1-285 < CLA>
R; Reinach, F.C.; MacLeod, A.R.
Nature 322, 648-650, 1986
A; Title: Tissue-specific expression of the A; Reference number: A24199; MUID:86311274;
A; Accession: A24199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Clayton, L.; Reinach, F.C.; Chumbley, G.M.; MacLeod, A.R. J. Mol. Biol. 201, 507-515, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: alternative splicing; coiled coil; muscle; skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-285 < REI >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: not compared with conceptual translation
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                        7 Match 10.7%; Score 112; DB 2; Local Similarity 23.5%; Pred. No. 1.8; 1es 52; Conservative 41; Mismatches 7;
                                                                              178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTFGIPED
                                                                                                                  EKAKIGRCETEERTRIA-----KELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQAN 159
                                                                                                                                                        R----ALKDEEKMELQEI-------QLKEAKHIAEEADRKYEEVARKLVIIEGDL
                                                                                                                                                                                                 KEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI 107
                                                                                                                                                                                                                                         LAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIEN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKEAANRWIDNIFAIKSWAKRKFGFEENKID 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERAEERAELSEGKC-----AELEEELKTVTNNLKSLEAQAEKYSQKEDKYEEEIKVLTDK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R----ALKDEEKMELQEI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK----HASL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                skeletal muscle - human
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                                                                          TEERABLAESKCSELEEELKNVTNNLKSLEAQAEKYSOKEDKYEEEIKILT 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.7%; Score 112; DB 22.7%; Pred. No. 1.8; Live 41; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human tropomyosin PMID:3018581
KLEKTIDDLED
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C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 15-Mar-2004
C;Accession: S49143
R;Frosch, P.M.; Hartmann, M.; Sygulla, L.; Margutti, P.; Frosch, M.
submitted to the EMBL Data Library, January 1994
A;Description: Identification of a cDNA clone from the larval stage of Echinococcus gran A;Reference number: S49143
A;Accession: S49143
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-559 <FRO>
A;Cross-references: EMBL:Z29489; NID:g509759; PIDN:CAA82625.1; PID:g509760
C;Superfamily: ezrin/radixin/moesin; protein 4.1 membrane-binding domain homology
F;12-293/Domain: protein 4.1 membrane-binding domain homology <B41>
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Search completed: July 27, 2005, 09:41:43
Job time : 42 secs
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Best Local Similarity
Matches 49; Conserv
                                                                                              395
                                                                                                                                           113 GRCETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANR 168
                                                                                                                                                                                                                                                                                            348 EKE-----
                                                                                                                                                                                                                                          61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSE-----GSQKHA--SLQKSIEK-AKI 112
                                                                                              NRKLKEETAASAEERNRLMAQRDEVQREVEAQK-----VAMAKKEAEKAQAEAELR 445
                                                                                                                                                                                                                                                                                                                                                                                                10.7%; Score 112; DB 2; Length 559; ilarity 27.8%; Pred. No. 3.7; Conservative 34; Mismatches 61; Indels
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Title:
Perfect score:
Sequence:
                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum DB seq length: 200000000
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                                              Database :
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Gapop 10.0 , Gapext 0.5
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UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                               1612378 seqs, 512079187 residues
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1047
1 MSKKKGLSAEEKRTRMMEIF......FEENKIDRTFGIPEDFDYID 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Query Query Query Query Atch Length DB ID Description Query Query	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	ហ	4.	ω	N	* <u>.</u>	Result No.	
Length DB ID Description 205 2 Q9BWT6 205 2 Q9DOA1 205 2 Q9DOA1 205 2 Q9DOA1 206 2 Q9EYD2 207 2 Q9EYB2 207			٠			4.		4.	•	•		•	168.5	175	197	206.5	221	266.5	277	332.5	340.5	340.5	340.5	349	427	440	462	644	948	954	1047	Score	
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Description Qbbwt6 homo Q8836 mus r Q9d0a1 mus r Q9d0a1 mus r Q9d0a2 arabi Q8gyd2 arabi Q8gyd2 arabi Q8gyd3 giara Q9739 giara Q7qtx0 giara Q7rh53 plass Q6g9f9 aeda Q6g15 deba Q7rh53 plass Q6g15 cand Q6g8 arabi Q6csx5 kluy Q9sze5 arabi Q6e679 noser Q7t268 mus r Q6awb1 homo Q6awb1 homo Q6iq37 homo Q6iq37 homo Q6iq37 homo Q6iq37 arati Q15315 gal1 Q5951 xenoy Q6pcj1 xenoy													YGT3_											YA53_S							1	ij	00000
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ALIGNMENTS

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XX MEDLINE-CZECH I; TISSUB-Mammary tumor;
XX MEDLINE-CZECH II; TISSUB-Mammary tumor;
XX MEDLINE-CZECH II; TISSUB-Mammary tumor;
XX MEDLINE-CZECH II; TISSUB-Mammary tumor;
XX Klausner R.D., Feingold E.A., Goruse L.H., Derge J.G.,
XX Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
XX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
XX Altschul S.F., Jordan H., Moore T., Massin G.M., Hong L.,
XX Altschuk L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altschuk C., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altschuk C., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
XX Altschuk C., Marisina K., Farmer G.J., Casavant T.L., Scheetz T.E.,
XX Altschuk C., Wollan T.B., Toshiyuki S., Carninci P., Prange C.,
XX Altschuk C., Wollan N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
XX Altschuk S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
XX Altschuk S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
XX Altschuk S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
XX Altschuk S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
XX Altschuk S., Worley K.C., Hale S., Garcia B.J., Lu X., Gibbs R.A.,
XX Altschuk S., Worley A.C., Shevchenko Y., Bouffard G.G.,
XX Allakesley R.W., Tuckman J., Worley R.M., Butterfield Y.S.,
XX Allakesley R.W., Tuckman J., Schmutz J., Myers R.M., Schein J.E.,
XX Allakesley R.W., Tuckman J., Schmutz J., Myers R.M., Schein J.E.,
XX Allakesley R.W., Sanchez A.,
XX Allakesley R.W., Sanchez
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01-OCT-2002
01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                                                   Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ
EMBL; BC027741; AAH27741.1; -
MGD; MGI:1924165; 2610034E18Rik.
InterPro; IPR005647; Mnd1.
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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"Generation and initial analysis
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c. Natl. Acad. Sci. U.S.A.
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                                                                                          Score 954;
                                                            Pred. No. 2.50
0; Mismatches
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STRAIN=C57BL/6J; TISSUB=Whole body;
STRAIN=C57BL/6J; TISSUB=Whole body;
STRAIN=C57BL/6J; TISSUB=Whole body;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka T., Tashiro H., Itoh M.,
Shibata K., Itoh M., Nishi K., Kitsunai T., Tashiro T., Harada A.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Hayashizaki Y.;
Yoneda Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DOA1;
Q9DOA1;
01-JUN-2001
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 days embryo whole body CDNA, RIKEN full
enriched library, clone:2610034E18 product:GAJ homolog.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-Whole body;

MEDLINE=20499374, PubMed=11042159; DOI=10.1101/gr.145100;

Carninoi P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,

Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected cDNAs
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The FANTOM Consortium,
the RIVEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851;
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636;
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STRAIN=C57BL/6J; TISSUE=Whole
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"High-efficiency full-length cDNA cloning.";
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
LA Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
R MGD; MGI:192416E. 2610021
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SEQUENCE FROM N.A.

C. STRAIN-Singapore local strain; TISSUB-Embryo;

C. STRAIN-Singapore local strain; TISSUB-Embryo;

X. Pubmed-1247793; DOI=10.1073/pnas.242603899;

X. Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X. Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K.,

X. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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X. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X. Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,

X. Hopkins R.F., Jordan H., Moore T., Wang J., Wang C.,

X. Hopkins R.F., Jordan H., Moore T., Wang J., Wang C.,

X. Hopkins R.F., Jordan H., Moore T., Wang J., Wang J.,

X. Hopkins R.F., Jordan H., Moore T., Wang J., Wang J.,

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Eukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii; T
Cyprinidae; Danio
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Pfam; PF03962; Mnd1; 1.
SEQUENCE 205 AA; 23909
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"Evolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource.";
Nat. Genet. 35:139-147(2003).
EMBL, AY223066, AAP06089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone ZZD1259 mRNA sequence.
Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
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Pfam; PF03962; Mndl;
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InterPro; IPR009058; Wing_hlx_DNA_bnd
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SEQUENCE 220 AA; 25176 MW; 90DEAA
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Pred. No. 1.2e-20;
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Matches 91
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Q8GYD2;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein At4g29170/F19B15_200 (Hypothet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2003) to the EMBL/GenBank/DDBJ EMBL; AK117713; BAC42364.1; -. EMBL; BT005435; AA063855.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M. Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C., Yu G., Yuan S., Carninci P., Chen P., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=At4g29170/F19B15_200; Synonyms=At4g29170;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
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InterPro; IPR005647; Mnc
Pfam; PF03962; Mnd1; 1.
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R.W., Ecker
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YA53_SCHPO

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01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence up

05-JUL-2004 (Rel. 44, Last annotation

Hypothetical protein C13A11.03 in chro

ORFNames=SPAC13A11.03;
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Q6H432;
Q5H432;
05-JUL-2004 (TrEMBLrel. 2
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05-JUL-2004 (TrEMBLrel. 2
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Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947.
MEDLINE-21848401; PubMed=11859360; DOI=10.1038/nature724; Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Erowh D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-2003) to the EMBL; AP006528; BAD26517.1; InterPro; IPR005647; Mnd1. Pfam; PF03962; Mnd1; 1. SEQUENCE 207 AA; 23900 MV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Oryza sativa nipponbare (GA3) clone:P0651G05.";
                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Schizosaccharomyces
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                                                                                                                                                                                                                                                           Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRKFGFEENKID---RTFGIPEDFDYI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAALEELKAVEQHIKKLKEELAAYADSDPAALEAMNDAIEVAHAAANRWTDNIFTLQQWC
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scomycota; Schizosaccharomycetes;
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Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Waltjens I., Vonstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Waltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Waltjens I., Vanstreels E., Rieger M., Schaefer M., Hilbert H.,
Waltjens I., Walter E., Moestl D., Hilbert H.,
Walter E., Moestl D., Hilbert H.,
Wanbutt R., Punnelle B.,
Walter P., Zimmermann W., Wedler H., Wambutt R., Punnelle B.,
Walter P., Zimmermann W., Wedler H., Wambutt R., Punnelle B.,
Walter P., Zimmermann W., Wedler H., Wambutt R., Punnelle B.,
Walter P., Zimmermann W., Wedler H., Reinhardt R.,
Walter P., Zimmermann W., Wedler H., Wanbutt R., Hurst S.M.,
Walter P., Zimmermann W., Wang Z., Hunt C., Moore K., Hurst S.M.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
A. Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
A. Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880 (2002).
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Best Local S
Matches 84
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Q8SUA9;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein ECU10_1600.
Name=ECU10_1600;
Encephalitozoon cuniculi GB-M1.
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InterPro; IPR009058; Wing_hlx_DNA_bnd
Pfam; PF03962; Mnd1; 1.
      MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thom
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wi
                                                                                                                                                                                          Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=284813;
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                                                                                                        STRAIN-GB-M1;
                                                                                                                                   SEQUENCE FROM N.A.
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Pred. No. 9e-14;
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RESULT 10
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                                                                                                                                                                                   Ramesh M.A., Malik S.B., Log Submitted (APR-2003) to the
                                                                                                                                                                                                                                           Giardia lamblia (Giardia intestinalis).
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
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05-JUL-2004
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InterPro; IPR005647; MndT.
InterPro; IPR009568; Wing_hlx_DNA_bnd
Pfam; PF03962; Mnd1; 1.
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Encephalitozoon cuniculi.";
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InterPro; IPR005647; Mndl.
InterPro; IPR00908; Wing_hlx_DNA_bnd.
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203 AA; 23743 MW;
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RESULT 12
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Matches 70
                                                                                                                                                        Q6Q9F9;
Q6Q9F9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7QTX0;
                                                05-JUL-2004 (TrEMBLrel. 27, Last annot MND1 domain containing protein. Aedes aegypti (Yellowfever mosquito). Bukaryota; Metazoa; Arthropoda; Hexapo Neoptera; Endopterygota; Diptera; Nema NCBI_TaxID=7159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
SEQUENCE FROM N.A.
TISSUE=Salivary gland;
Chandra P.K., Wikel S.K.;
                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLP_76_12374_11763.
Giardia lamblia ATCC 50803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Diplomonadida;
NCBI_TaxID=184922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005647; Mnd1.
InterPro; IPR009058; Wing_hlx_DNA_bnd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morrison H.G., McArthur A.G., Adam R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=WB C6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
L; AACB01000100; EAA38463.1; -.
                                                                                                                                                                                                                                                                                      123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF03962; Mnd1;
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                                                                                                                                                                                                                                                             GFEENKIDRTFGIPEDFDYID
                                                                                                                                                                                                                                                                                      KEKLALQVKLEEQRGTFRDLLKNDPDVAQKLRNYTDIAKQEANLWTDNIFCLQKYMLTKL
                                                                                                                                                                                                                                                                                                                                                              IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLA 124
                                                                                                                                                                                                                                                                                                                                                                                                                 KGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFEENKIDRTFGIPEDFDYID
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                                                                                                                                                                                                                                      QMDKKTVSTALGITGEFDYLE
                                                                                                                                                                                                                                                                                                              KELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWIDNIFAIKSWAKRKF
                                                                                                                                                                                                                                                                                                                                      IGASTYYWCFASKRSQAARTELARLQKALEEQTNFIDKATARIEELKVGREETEERSSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QMDKKTVSTALGITGEFDYLE
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                                                                                                                                                                                                                                                                                                                                                                                         KGTSLDEKKERLLEEMLKRGEIYSNKTIETLS-KPTGISSMVIKNVLQALVNEDLVDTDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23278 MW; CC0625DCDC4158C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.5%;
                                                                Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hexamitidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                            46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
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Pred. No. 2.0
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                                                                          Hexapoda; Insecta; Pterygota;
                                                                                                                                                                      179
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                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            84;
                                                                Culicoidea; Aedes
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RESULT 13
Q7RH53
ID Q7RH5
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Best Local S
Matches 66
                                                                                                                                                           Query Match
Best Local :
                                                                                                                                             Matches
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Q7RH53;
01-MAR-2004
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EMBL; AY55
                                                                                                                                                                                                                                                                                                                                                            PubMed=12368665; DOI=10.1038/nature01099;
Carlton J.M., Angiuoli S.V., Suh B.B., Kooi T.W., Pertea M.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium yoelii yoelii.
Bukaryota; Alveolata; Api
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005647; Mnd1.
Pfam; PF03962; Mnd1; 1.
SEQUENCE 179 AA; 20900 MW;
                                                                                                                                                                                                                   preliminary data.
EMBL; AABLO1001237; EAA15959.1;
InterPro; IPR005647; Mndl.
Pfam; PF03962; Mndl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=PY04140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens GAJ, putative.
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                        Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                    "Genome sequence and comparative analysis of the model parasite Plasmodium yoelii yoelii.";
                                                                                                                                                                                                                                                                                                                                                      Carucci D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                              CAUTION: The sequence shown here is derived EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ whole genome shotgun
116
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                                                                                     N
                                                                                                                                                           Similarity
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ETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFA 175
                                                                                                          KKKGLSABEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEMFEKLNTLKEKQKQLSSKLDKAKLKQSDQNSVDKMNRNLPDLHDAANRWDGTTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSK-KKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTRLAKELSSLRDQREQLKAEVE--KYKDCDPQVVEEIRQANKVAKEAANRWTDNIFA 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKVGSQNVFWILKTEESSILQNKYQELKDKKEEYEEMAQAEKENYAELENSLS-----L
                                                      ERIGTSNYYWAFPSKALHARKHKLEVLESQLSE-----GSQKHASLQKSIEKAKIGRC 115
                                                                                   KKKGKSNEDKKLILYDIMLESESFFILKELEALAPK-KGIRSIFVKDLIQQLIDDNKIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSKRKKGISAGEKKSIVLEIFHQSKEFYQLKDVERIAVKDKGLREQVVKEILQNLVDEGQ
                                                                                                                                                                                                    962; Mnd1;
196 AA; 2
                                                                                                                                             Conservative
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                                                                                                                                                                                                       23066 MW;
                                                                                                                                                           26.5%;
29.7%;
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26,
                                                                                                                                             52;
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Last annotation updat
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                                                                                                                                                           Score 277;
Pred. No. 1.
                                                                                                                                                                                                       7FD8820707329074 CRC64;
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                                                                                                                                           Mismatches
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                                                                                                                                                           DB 2;
..9e-09;
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                                                                                                                                           14;
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                                                                                                                                           Gaps
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RESULT 14
Q6BQL5
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Best Local S
Matches 61
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Q6BQL5;
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope;
submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382137; CAG87731.1; -.
InterPro; IPR005647; Mnd1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Besisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Besisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Strub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P. Schrief J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF03962; Mnd1;
NON_TER 1
SEQUENCE 211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bouchier C., Caudron B., Scarp Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; NCBI_TaxID=284592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=DEHA0E04994g;
Debaryomyces hansenii CBS767.
Eukaryota; Fungi; Ascomycota;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to CA3413 | IPF9239 Candida albicans IPF9239 unknown function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature
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                                                                                                                                                                           ----EERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEBIRQANKVAKEAANRWTDNI
                                                                                                                                                                                                                                          KCGTTNLYWCF-----KFDKIKTLQTQYNNYQNKLKEKQLERDQLIEKIQLGKLQRLV
                                                                                                                                                                                                                                                                                             RIGTSNYYWAFPSKALHARKHKLEVLESQLS--EGSQKHASLQKS--IEKAKIGRCET--
                                                                                                                                                                                                                                                                                                                                                         KKGLSAEDKKEKLYEFFNQSHTFYTLKEIEKEGSKYAKISSMLIKDIVQQLIDDNLINCE
                                                                                                                                                                                                                                                                                                                                                                                                                  KKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCE
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ESMIYYFTKVSSATIEELDLRSELGIPSEF
                                                                                                                  KSDFGNRHKLIDQFTCLSKRKLHLEEELLKYGDNDPQLIQTLDEKNVHLILAIETFTDDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24831 MW;
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29.0%; Pred. No. 8.8e-09;
cive 55; Mismatches 75
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Q75CH5;
05-JUL-2004
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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Brachat S., Voegeli S.E.,
Philippsen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales; Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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184
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NCE 225 AA;
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                                                                                                            SEGVSYTROALLTEHDELGROLAALQSAYRKLEDTKWDETKIDSYCRGVRSKLEQLDKIT
                                                                                                                                                                                                                               SVEKCGNVNVYWCFKNQLVGKMCTEMQAMKARSEESQVRLQELQAAINSEKKHARAAAFR
                                                       DNIFAIKSWAKRKFGFEENKIDRTFGIPEDFD
                                                                                                                                                                 CETEERTR - - LAKELSSLRDQREQLKAEVEKYKDC - - DPQVVEEIRQANKVAKEAANRWT
                                                                                                                                                                                                                                                                                                                                           KRAVVTLAEKKARVLKFFQEEHSIYSIKDLEKLIPKKCAGVSSMLVKDIVQQLIDEDGLI
  DNIEVIVSFLMRRHAVSRAELAAALDMPEEFE
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Pred. No. 5.3e-06;
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Search completed: July 27, 2005, 09:40:57 Job time : 176 secs

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OM protein - pr Run on: Title: Perfect score: Sequence: Scoring table:	GenCore v rright (c) 1993 - search, using sw 27, 2005, 09:29:4 .087-190-3 CKGLSAEEKRTRMMEIF
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0 0	513545 seqs, 74649064 residue hits satisfying chosen parame
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Post-processing:	: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	Issued_Patents_AA:* 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:* 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:* 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:* 5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:* 6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
Pred. No. score gre and is de	vo. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
Result No. Score	\$ SUMMARIES Query Match Length DB ID Description
	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
8 112.5 9 112 10 111 11 110 12 110 13 109.5	630 4 US-09-248-796A-2027 284 4 US-09-914-259-43 1937 4 US-09-918-092-918 284 4 US-09-914-259-46 284 4 US-09-914-259-49 170 4 US-09-438-185A-708
	284 4 US-09-914-259-51 Sequence 817 4 US-09-248-796A-20276 Sequence 281 4 US-09-914-259-63 Sequence 284 4 US-09-167-206-10 Sequence 284 4 US-09-914-259-40 Sequence
	284 4 US-09-914-259-48 Sequence 284 4 US-09-914-259-50 Sequence 284 4 US-09-914-259-41 Sequence 284 4 US-09-914-259-41 Sequence 534 4 US-09-103-664A-2 Sequence
	1786 3 US-08-9/3-465-8 Sequence 224 2 US-08-772-255-16 Sequence 224 5 PCT-US95-08565-16 Sequence 224 4 US-10-164-595-34 Sequence 245 4 US-10-164-595-36 Sequence

Sequence 4959, Application US/09621976
; Sequence 4959, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
 APPLICANT: Dumas wilne Edwards, J.B.
 APPLICANT: Jobert, S.
 APPLICANT: Glordano, J.Y.
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4959
LENGTH: 127
; Type: PAT
; ORGANISM: Homo sapiens
US-09-621-976-4959

45	44	4 3	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28
99.5	100	100	100.5	101.5	101.5	102	102	102	102	102	102	102	102	104	104	105	105
9.5	9.6	9.6	9.6	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.7	9.9	9.9	10.0	10.0
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US-08-714-741-42	US-08-923-992A-10	US-08-923-992A-4	US-09-914-259-59	US-09-538-092-1252	US-09-595-684B-31	US-09-949-016-8888	US-09-538-092-901	US-09-914-259-24	US-08-330-515-3	US-07-813-584A-3	US-09-914-259-57	US-09-914-259-47	US-09-914-259-45	US-09-949-016-11104	US-09-538-092-915	US-09-914-259-60	US-09-914-259-64
	Sequence 10,	Sequence 4, 1	Sequence 59,	Sequence 1252	Sequence 31,	Sequence 8888,	Sequence 901,	Sequence 24,	Sequence 3, 1	Sequence 3, 1	Sequence 57,		Sequence 45,	Sequence 111	Sequence 915	Sequence 60,	Sequence 64,
App1	Appl	Appli	Appl	Αp	31, Appl	Ap	App	Appl	Appli	Appli	Appl	Appl	Appl)4, A	App	App1	App1

ALIGNMENTS

RESULT 1 US-09-621-976-4959

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US-09-248-796A-14485
Sequence 14485, Application US/09248796A

Patent No. 6747137

GENERAL IMPORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13
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Best Local Similarity 89.6%;
Matches 120; Conservative 5
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118 ----IKLSGMQEER 127
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US-09-914-259-65

Sequence 65, Appl

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; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14203
US-09-538-092-1321
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US-09-538-092-1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version SEQ ID NO 1321
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PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14485
LENGTH: 260
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Best Local 9
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILLNG DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Protein-Protein Complexes FILE REFERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Giot, Loic APPLICANT: Mansfield,
                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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390
                                111 KIGRCET--EERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANR 168
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                                                                      331 LEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALVRMRDLSSSEKQEHVKLQKLMEK-
                                                                                                                                            271 ARKEAKEALEAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKERVDELTTD
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Similarity 27.1%;
59; Conservative 4
                                                                                                      CERI-----GTSNYYWAFPSKALHAR-KHKLEVLESQLSEGSQKHASLQKSIEKA 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CKDETGVRNQTHERASKIRFCDQSLERIDSIQSQLQSLKDSES--VE----NLVTSLAF
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KNQELEVVRQQRERLQEELSQAESTIDELKEQVDAALGAE-EMVEMLTDRNLNLEEKVRE
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                  12.8%;
                                                                                                                                                                                                                    43;
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Pred. No. 8.8e-11;
"'ematches 75;
                                                                                                                                                                                                                  Score 134.5; DB 4;
Pred. No. 0.00028;
3; Mismatches 106;
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                                                                                                                                                                                                                                                     Length 1270;
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                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 752-59
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hanson, No. 6232460man D. REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: LUD 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,324B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15-July-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS
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ZIP: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/892,702
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650 LESAKOKFGEITDTYOKEIEDKKI
                                        178 -SWAKRKFG-----FEENKI 191
                                                                                                                  137 LKAEVEKYKD-CD-----PQVVEEIRQANKVAKE--AANRWTDNIFAIK-----
                                                                                                                                                      532 QETSDMTLELKNQQEDINNNKKQEERMLKQIE--NLQETETQLRNELEYVREELKQKRDE
                                                                                                                                                                                                                                   472 QAREKEVHDLEIQLTAITTSEQYYSKEVKDLKTELENEKLKNTELTSHCNKLSLENKELT 531
                                                                                                                                                                                                                                                                                                               413 QKKSSELBEMTKLTNNKEVELEELKKVLGEKETLLYENKQFEKIAEELKG-TEQELIGLL 471
                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                       52 QSL---VDDGMVDCERIGTSNYYWAFPSKAL--------HARKHKLEVLE--
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                                                                            VKCKLDKSEENCNNLRKQVENKNKY I EELQQENKALKKKGTAESKQLNVYE I KVNKLELE
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Methods For Diagnosis And Treating Cancers,
And Methods For Identifying Pathogenic Markers In
                                                                                                                                                                                                                                                                                                                                                                                                            11.2%; Score 117; DB 3; Length 976; 23.9%; Pred. No. 0.0099;
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                                                                                                                                                                                            --SQLSEGSQXHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQREQ 136
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RESULT 5

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FILE REFERENCE: 15966-542
CURRENT FILING DATE: 2000-03-29
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CURAPATS SQFFORMATTER TO SEQ ID NO 1339
SEQ ID NO 1339
                                                        ; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-914-259-55
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                                                                                                          APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT FILING DATE: 2000-11-21
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 284
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Makowski,
                                                                                                                                                                                                                                                                                                                                              Sequence 55, Appl Patent No. 649533
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Query Match
Best Local Similarity
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APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q15431
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -SWAKRKFG-----FEENKI 191
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                                                                                                                                                                                                                                                                                                                                                              Application US/09914259
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23.9%;
10.9%;
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Pred. No. 0.0099
Score 114; DB 4; Pred. No. 0.0037;
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                  Length 284;
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RESULT 8
US-09-248-796A-20275
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US-09-914-259-62
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Sequence 20275, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT PILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version SEQ ID NO 62
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Best Local (
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APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STACED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 62, Application US/09914259
Patent No. 6495336
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                                                                                                                                                                                                                                                                                          216
                                                                                                                                                                                                                                                                                                                                                                      161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 ---ERLATALQKLEEAEKAADESERGMKVIESRAQKDEEKMEIQEIQLKEAKHIAEDADR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 EVARKLVIIESDLERAEERÄELSEGKC-----AELEEELKTVTNNLKSLEAQAEKYSQKE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 SERGM-----KVIESRAQKDEEKMEIQEIQLKEA--KHIAEDADRKYB 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ---GMVDCERIGTSNYYWAFPSKALHAR----KHKLEVLESQLSEGSQKH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 VDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK-----
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                                                                                                                                                                                                                                                                                                                              DCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENKID 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAEKKATDAEADVASLNRRIQLFEEELDRAQ----ERLA----TALQKLEEAEKAADE
                                                                                                                                                                                                                                                                                          QKEDKYEEEIKVLSDKLKEAETR-----ABFAERSVTKLEKSID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKEKLIRASEDERDRVLEELHKAEDSILAAD-ETAAKAEADVASINRRIQIVEEELDRAQ 103
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                                                                                                                                                                                                                                                                                                                                                                                                           -----HASLOKSIEKAKI--GRCETBERTRLAKELSSLRDQREQLKAEVEKYK 145
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Pred. No. 0.0042;
""matches 78;
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                                                                                                                      RELATING TO CANDIDA ALBICAN
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RESULT 10
US-09-538-092-918
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US-09-914-259-43
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PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 180
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 43, Application US/09914259 Patent No. 6495336
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Best Local S
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Best Local 9
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APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
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TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo
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Local Similarity 23.8%;
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les 52; Conserv
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                                                                            230 DKLKEAETRAE---FAERSVA--
                                                                                                                                                                                                                                                                                                        73
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                                                                                                                                                                                                                                                                 48 KEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI 107
                                                                                                                                                                                                                                                                                                                                            1 MSKKKGLSAEEK---RTRMMEIFSETKDVFQ-----LKDLEKIAPK-EKGITAMSV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGIT--AMSVKEVLQSLVDDGMV
                                                                                                              KVAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTFGIPED 200
                                                                                                                                                                                      EKAKIGRCETEERTRLA-----KELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQAN 159
                                                                                                                                                                                                                              R----ALKDEEKMELQEI------QLKEAKHIAEEADRKYEEVARKLVIIEGDL
                                                                                                                                                                                                                                                                                                      LAEKKAADAEAEVASINRRIQIVEEEIDRAQERLATAIQKIEEAEKAADESERGMKVIEN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N---DN-----SGAKKELLEKVSKLE 344
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                                                                                                                                                     ER-----TEERAELAESKCSELEEELKNVTNNLKSLEAQAEKYSQKEDKYEEEIKILT
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   41;
                                                                                                                                                                                                                                                                                                                                                                             Score 112; DB 4; Le
Pred. No. 0.0059;
Mismatches 72;
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                                                                          -KLEKTIDDLED
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 284;
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CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 284
TYPE: PRT
ORGANISM: Brachydanio rerio
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US-09-914-259-46
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SEQ ID NO 918
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APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED AS
FILE REFERENCE: 8471-010-999
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PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
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CURRENT FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P13535
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   73
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                                                                    1 MSKKKGLSAE---EKRTRMMEIFSETKDVFQ-----LKDLEKIAPK-EKGITAMSV 47
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23.1%; Pred. No. 0.096;
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                                                                                                                                             44;
                                                                                                                                             Score 110; DB 4;
Pred. No. 0.0092;
14; Mismatches 72;
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88
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US-09-438-185A-708
; Sequence 708, Application US/09438185A
; Patent No. 6822071
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Mayie, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/108,606
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR APPLICATION NUMBER: US 60/128,606
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US-09-914-259-49
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LENGTH: 284
TYPE: PRT
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Best Local
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APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STACED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-99
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILLING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
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-09-914-259-49.
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                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ETR-----AEFAERTVAKLEKSID
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                                                                                                                                                                                                                                                                                                                                                                                                                                    254
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RESULT 15
US-09-248-796A-20276
; Sequence 20276, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
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APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 284
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 708
LENGTH: 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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ORGANISM: Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: CPn0706
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                                                                                                                                                                          166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 RTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANK 160
                                                                                                                                                                                                                                                                                                                              48 KEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 EEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 ----SDAVLQIKSYIKVVAVQLSEEEEKVNKQKEVVLAASKELEKAEVNLAKRRKEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 YYWAFPSKALHARKHKLEVLESQLSE-----GSQKHASL--QKSIEKAKIG----RCETEE 119
                                                                                                                                                                                                                                                                                                                                                                  73 LSDKKATDAEGDVASLNRRIQLVEEELDRAQERLSTALQKLEEAEKAADESERGMKVIEN 132
                                                                                                                                                                                                                                                                                                                                                                                                        1 MSKKKGLSAE---EKRTRMMEIFSETKDVFQ-----LKDLEKIAPK-BKGITAMSV 47
                                                                                                                                                                          ANRWIDNIFAIKSWAKRKFGFEENKID 192
                                                                                                                                        ETR-----AEFAERTVAKLEKSID
                                                                                                                                                                                                              ERAE-ERAELSESKCAELEEELKTVINNLKSLEAQAEKYSQKEDKYBEEIKVLTDKLKEA
                                                                                                                                                                                                                                                  EKAKIGRCETEER--TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVBEIRQANKVAKEA 165
                                                                                                                                                                                                                                                                                        R----ALKDEEKMELQEI------QLKEAKHIAEEADRKYEEVARKLVIIEGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTRLHKEEWMKEALKEEARAE-EKEQDEMGQLLFQLRQKKK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEKR-RILEIEQE-----KLREKEAERDKVKNHYMQKIQQ-LRDLLDEGTT---
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23.7%; Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 109.5; DB Pred. No. 0.0052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                            176
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20276
LENGTH: 817
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20276
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Search completed: July 27, 2005, 09:42:31 Job time : 43 secs
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                                                                                                                                                                                       9 AEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVK--EVLQSLVD---DGMVDCE 63 ||||: :: | :| :: | :| :| :| | :| 426 AEEKQV-LLDEKKENQDRIDTEEAEKIAARKQELEELQAEKDEILKPTLDELKEESAKLE 484
                                                                                              599 KVK-----DEHKINSE--LPE 612
                                                                                                                                            179 WAKRKFGFEENKIDRTFGIPE 199
                                                                                                                                                                                                                                                                                           485 EVTNARDELANEVKASEDLNKEYEEKLAELESKLQEAKNDIEKYTTDIEEA-----TAK 538
                                                                                                                                                                                                                                                                                                                                 64 RIGTSNYYWAPPSKALH----ARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEE 119
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Result
No.
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          1036.5
1036.5
1011
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                                                                              1047
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1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

21: /cgn2_6/ptodata/1/pubpaa/US10A_PUB.pep:*

22: /cgn2_6/ptodata/1/pubpaa/US10A_PUB.pep:*

23: /cgn2_6/ptodata/1/pubpaa/US10A_PUB.pep:*

24: /cgn2_6/ptodata/1/pubpaa/US10A_PUB.pep:*

25: /cgn2_6/ptodata/1/pubpaa/US10A_PUB.pep:*
          US-10-087-190-3
1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1741741 seqs, 388992284 residues
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Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                 Length
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          15
15
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15
  US-09-799-250-2

US-10-087-190-3

US-10-087-190-14

US-10-087-190-20

US-10-087-190-21

US-10-087-190-21

US-10-087-190-61

US-10-087-190-61

US-10-087-190-44

US-10-087-190-44

US-10-087-190-44

US-10-087-190-44

US-10-087-190-24
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511.176 Million cell updates/sec
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Sequence 2, Appli
Sequence 3, Appli
Sequence 14, Appli
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 61, Appl
Sequence 61, Appl
Sequence 44, Appl
Sequence 45, Appl
Sequence 24, Appl
Sequence 24, Appl
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17	10	14	16	15	14	14	15	10	16	16	16	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	15	10	15	15	15	15	15
-10-732-923-3	9-981-151A-	-10-032-585-764	-10-408-765A-209	-10-424-599-1926	-10-083-357-1	US-10-106-698-5443	-10-087-190-2	-09-799-250-	-10-437-963-16290	-10-437-963-16289	-10-425-115-25301	-10-087-190-	-10-087-190-1	-10-087-190-	-10-087-190-	-10-087-190-	-10-087-190-	-10-087-190-5	0-087-190-5	-10-087-190-	0-087-190-	-10-087-190-5	-10-087-190-6	-10-087-190-	-10-087-190-1	-10-087-190-1	-10-087-190-	-09-799-250-	-10-087-190-	-10-087-190-6	-10-087-190-6	-10-087-190-	0-087-190-1
equence 3300,	e 48,	equence 764	equence 2096,	equence 192650	equence 1304,	quence 544	equence 25, Ap	equence 5, App	e 162901	equence 162	equence 253	e 46, App	equence 15, App	equence 5,	equence 47, App	equence 16, App	equence 7, Appl	e 55,	equence 54, App	equence 17, App	equence 9,	equence 53,	equence 63,	equence 62,	equence 18,	equence 11,	equence 23, App	equence 4,	equence 69, App	equence 68,	equence 67,	quence 19,	equence 13,

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/799,250
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 719
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 205
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250-2
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 205; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09799250 Publication No. US20030032087A1
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                               APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121P1F1: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.34US01
61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER 120
                                                        1 MSKKKGLSABEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
                                  MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
                                                                                                                                                                                                                                                                                                                                                                                                       Mary Faris
Daniel E.H. Afar
                                                                                                        0
                                                                                                    Score 1047; DB 10
Pred. No. 3.8e-78;
D; Mismatches 0;
                                                                                                                                     DB 10;
                                                                                                        Indels
                                                                                                                                       Length
                                                                                                      0
                                                                                                    Gaps
                                                                   60
                                    60
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APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 08/779,250
P
Sequence 14, Application US/10087190
Publication No. US20030223997A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
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APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia N
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sin Matches 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10087190 Publication No. US20030223997A1
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Afar, Daniel E. H.
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Pred. No. 3.8e-78;
); Mismatches 0;
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SOPTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 14; LENGTH: 205; TYPE: PRT; ORGANISM: Homo Sapiens
US-10-087-190-14
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                                                                                                                                                          ; TYPE: PRT; ORGANISM: Homo Sapiens US-10-087-190-20
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                                                                                                                                                                                                                                           SEQ ID NO 20
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                                                                               Matches
                                                                                                                    Query Match
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APPLICANT: Jakobovitz, Aya
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION UNMERS: US 09/779,250
PRIOR PILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
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APPLICANT: Challita-Eid, F
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION STATE OF SEQ ID NOS: 69
NUMBER OF SEQ ID NOS: 69
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APPLICANT:
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SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                    LENGTH: 205
                                                                                                  Local Similarity
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                  MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
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MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
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Afar, Daniel E. H.
                                                                           100.0%; Score 1047; DB 15; ilarity 100.0%; Pred. No. 3.8e-78; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                              Version
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: NUTLEIC 121P1F1 USEFUL IN TREATMENT AND DETECTION OF FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US/9/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 205
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US-10-087-190-21
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Best Local S
Matches 205
                                                          Sequence 22, Application US/10087190
Publication No. US20030223997A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
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ORGANISM: Homo Sapiens
-10-087-190-21
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APPLICANT: Challita-Eic
                              APPLICANT:
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Local Similarity 100.0%; Pred. No. 3.8e-78;
nes 205; Conservative 0; Mismatches 0;
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Afar, Daniel E. H.
Ge, Wangmao
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Hubert, Rene S.
Faris, Mary
Afar, Daniel E. H.
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                                           Arthur B.
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US-10-087-190-61
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E. H.
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APPLICANT: Jakobovitz, Aya
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: RATITLED 1212171 USEFUL IN TREATMENT AND DETECTION OF CANCER
TITLE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
SEQ ID NO 22
SEQ ID NO 22
SEQ ID NO 23
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APPLICANT: Jakobovitz, Aya
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121PIF1 USEFUL IN TREATMENT AND DETECTION OF CANCER
TITLE REFERENCE: 51158-20034.20
CURRENT FILING NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER: OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 61
LENGTH: 2005
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Matches
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Best Local Similarity 100.0%; 1
Matches 205; Conservative 0;
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                                                                                                                             Query Match
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ORGANISM: Homo
                                                                                                        Local Similarity
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                         MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
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                                                                                   100.0%; Score 1047; DB 15; ilarity 100.0%; Pred. No. 3.8e-78; Conservative 0; Mismatches 0;
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Pred. No. 3.8e-78;
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Sequence 44, Application US/10087190
Publication No. US20030223997A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
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US-10-408-765A-1821
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CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1821
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Best Local Similarity
Matches 205; Conserv
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APPLICANT: Gibson, Bradford w.
APPLICANT: Taylor, Steven w.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
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APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
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100.0%; Pred. No. 3.8e-78;
vative 0; Mismatches 0;
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US-10-087-190-45
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US-10-087-190-44
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; ORGANISM: Homo Sapiens
US-10-087-190-45
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APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, P
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 206
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SOPTMARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 206
TYPE: PRT
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Best Local Similarity
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TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
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 DCERIGTSNYYWAFPSKALHARKHKLEVLESQ-LSEGSQKHASLQKSIEKAKIGRCETEE 119
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                                    MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
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Afar, Daniel E. H.
                                                                                                            Conservative
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Pred. No. 2.8e
0; Mismatches
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Pred. No. 2.8e
0; Mismatches
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PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR PILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
ENOTH: 198
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-24
                                                 Sequence 13, Application US/10087190; Publication No. US20030223997A1; GENERAL INFORMATION: APPLICANT: Agensys, Inc.; APPLICANT: Challita-Eid, Pia M.; APPLICANT: Hubert, Rene S.; APPLICANT: Raitano, Arthur B.
                                                                                                                                                                           RESULT 12
US-10-087-190-13
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US-10-087-190-24
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Best Local Similarity 100.0%; Properties 198; Conservative 0;
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 APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
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                                                                                                                                                                                                                                                                                                                                         KELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKF 184
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Faris, Mary
Afar, Daniel E. H.
Ge, Wangmao
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Afar, Daniel E. H.
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Raitano, Arthur B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1011; DB 15; pred. No. 3.3e-75; 0; Mismatches 0;
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; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTMARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 190
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US-10-087-190-19
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; ORGANISM: Homo
US-10-087-190-13
                                                                                                                                                        US-10-087-190-19
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E. H.
                                                                                                                                                                                                                               APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121PIF1 USEFUL IN TREATMENT A
FILE REFERENCE: 51158-20034.20
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 19
SEQ ID NO 19
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Best Local (
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                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo
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                  16 MMEIFSETKOVFOLKDLEKIAPKEKGITAMSVKEVLOSLVDDGMVDCERIGTSNYYWAFF
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MMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNYYWAFP
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                                                                         93.1%; Score 975; DB 15;
100.0%; Pred. No. 2.9e-72;
tive 0; Mismatches 0;
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                                                                                                                Length 190;
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Sequence 68, Application US/10087190
Publication No. US20030223997A1
GENERAL INFORMATION:
APPLICANT: Ageneys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E. H.
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US-10-087-190-68
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US-10-087-190-67
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Best Local S
Matches 190
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
TILE REFERENCE: 51158-20034.20
CURRENT PILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 190
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APPLICANT: Challita-Eid, Pia M
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E. H.
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ORGANISM: Homo Sapiens
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Afar, Daniel E. H.
Ge, Wangmao
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Faris, Mary
Afar, Daniel E. H.
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; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1P1 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: ENTITLED 121P1P1 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 68
LENGTH: 190
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Search completed: July 27, 2005, 09:54:35 Job time : 157 secs
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